Supplementary Table 2. Analysis of localization of Pita/ZIPIC/Zw5 in comparison with TADs in the Hi-C map.

(A) Proportions of peaks falling into inter-TADs and TADs (data on four cell lines). To avoid partial overlaps between TADs and inter-TADs, the inter-TAD regions were explicitly subtracted from TADs. The overlaps with peaks for TADs and inter-TADs are comparable, but the total length of inter-TADs is nearly half smaller than that of TADs.
(B) Observed and expected proportions of peaks falling into inter-TADs of a given total length (relative to the total mappable genome size). Binomial P-value for peaks-in-interTADs enrichment (chance to observe no less than the given number of peaks in interTADs of the fixed total length and fixed total peaks count for a particular TF).

(A)

		Cell line							
		Bg3		**Kc167**		**OSC**		**S2**	
TF	**peaks**	**TAD**	**inter-TAD**	**TAD**	**inter-TAD**	**TAD**	**inter-TAD**	**TAD**	**inter-TAD**
CP190	7960	0,48	0,51	0,51	0,48	0,49	0,50	0,53	0,46
Pita	1845	0,41	0,54	0,45	0,50	0,41	0,54	0,47	0,48
ZIPIC	575	0,24	0,63	0,30	0,57	0,22	0,65	0,30	0,58
Zw5	695	0,27	0,66	0,34	0,58	0,30	0,62	0,35	0,57

(B)

		Cell line							
		Bg3 inter-TAD		**Kc167 inter-TAD**		**OSC inter-TAD**		**S2 inter-TAD**	
TF	**peaks**	**fraction**		**fraction**		**fraction**		**fraction**	
CP190	7960	0,51	*0,36*	0,48	*0,34*	0,50	*0,36*	0,46	*0,32*
Pita	1845	0,54	*0,36*	0,50	*0,34*	0,54	*0,36*	0,48	*0,32*
ZIPIC	575	0,63	*0,36*	0,57	*0,34*	0,65	*0,36*	0,58	*0,32*
Zw5	695	0,66	*0,36*	0,58	*0,34*	0,62	*0,36*	0,57	*0,32*
		observed	*expected*	observed	*expected*	observed	*expected*	observed	*expected*

		Cell line							
		Bg3 inter-TAD		**Kc167 inter-TAD**		**OSC inter-TAD**		**S2 inter-TAD**	
TF	**peaks**	**count**	**P-value**	**count**	**P-value**	**count**	**P-value**	**count**	**P-value**
CP190	7960	4053	0,00E+00	3807	0,00E+00	3988	0,00E+00	3690	0,00E+00
Pita	1845	1000	0,00E+00	922	0,00E+00	988	0,00E+00	893	0,00E+00
ZIPIC	575	363	0,00E+00	328	0,00E+00	371	0,00E+00	331	0,00E+00
Zw5	695	456	0,00E+00	406	0,00E+00	434	0,00E+00	397	0,00E+00

cell line	**total inter-TAD length**	**genome fraction**
Bg3	43660000	0,364
Kc167	40560000	0,338
OSC	43060000	0,359
S2	38920000	0,324